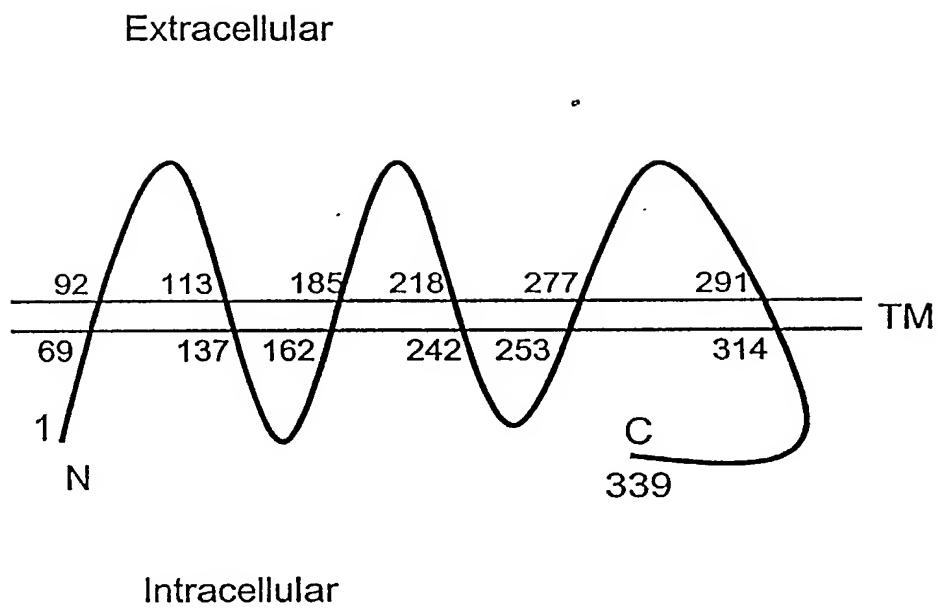


## FIG. 1A

(SEQ ID NO:1

↓  
 1 GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT ATA GAA  
 (SEQ ID NO:2)→ M E S R K D I T N Q E E L W K M K P R  
 61 TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA ATG AAG CCT AGG  
 R N L E E D D Y L H K D T G E T S M L K  
 121 AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA GAG ACC AGC ATG CTA AAA  
 R P V L L H L H Q T A H A D E F D C P S  
 181 AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCA CAT GCT GAT GAA TTT GAC TGC CCT TCA  
 E L Q H T Q E L F P Q W H L P I K I A A  
 241 GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT  
 I I A S L T F L Y T L L R E V I H P L A  
 301 ATT ATA GCA TCT CTG ACT TTT CTT TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA  
 T S H Q Q Y F Y K I P I L V I N K V L P  
 361 ACT TCC CAT CAA CAA TAT TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA  
 M V S I T L L A L V Y L P G V I A A I V  
 421 ATG GTT TCC ATC ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC  
 Q L H N G T K Y K K F P H W L D K W M L  
 481 CAA CTT CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA  
 T R K Q F G L L S F F A V L H A I S  
 541 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT GCT GTA CTG CAT GCA ATT TAT AGT  
 L S Y P M R R S Y R Y K L L N W A Y Q Q  
 601 CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG GCA TAT CAA CAG  
 V Q Q N K E D A W I E H D V W R M E I Y  
 661 GTC CAA CAA AAT AAA GAA GAT GCC TGG ATT GAG CAT GAT GTT TGG AGA ATG GAG ATT TAT  
 V S L G I V G L A I L A L L R A V T S I P  
 721 GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT CTG TTG GCT GTG ACA TCT ATT CCA  
 S V S D S L T W R E F H Y I Q S K L G I  
 781 TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA TTT CAC TAT ATT CAG AGC AAG CTA CGA ATT  
 V S L L L G T I H A L I F A W N K W I D  
 841 GTT TCC CTT CTA CTG GGC ACA ATA CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT  
 I K Q F V W Y T P P T F M I A V F L P I  
 901 ATA AAA CAA TTT GTA TGG TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT  
 V V L I F K S I L F L P C L R K K I L K  
 961 GTT GTC CTG ATA TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG  
 I R H G W E D V T K I N K T E I C S Q L  
 1021 ATT AGA CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG  
 TAG ATT TAC TGT TTA CAC ACA TTT TTG TTC ATT ATT GAT ATA TTT TAT CAC CAA CAT TTC  
 AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA AA  
 1141

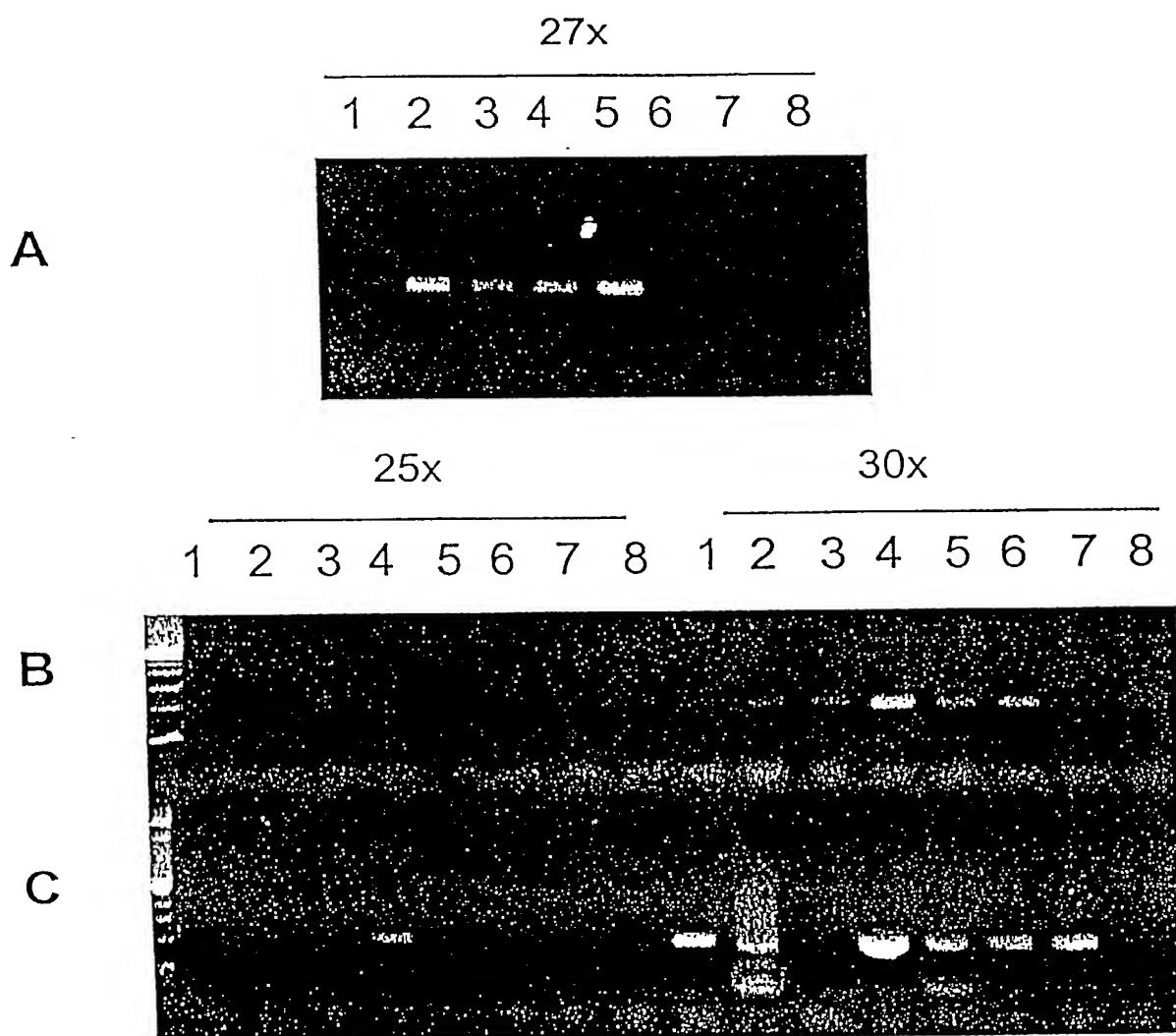
**FIG. 1B**



## FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG  
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT  
AAC AGC AAG 3' (SEQ ID NO:3)

**FIG. 2**



**Panels:**

**A**

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

**B**

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

**C**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

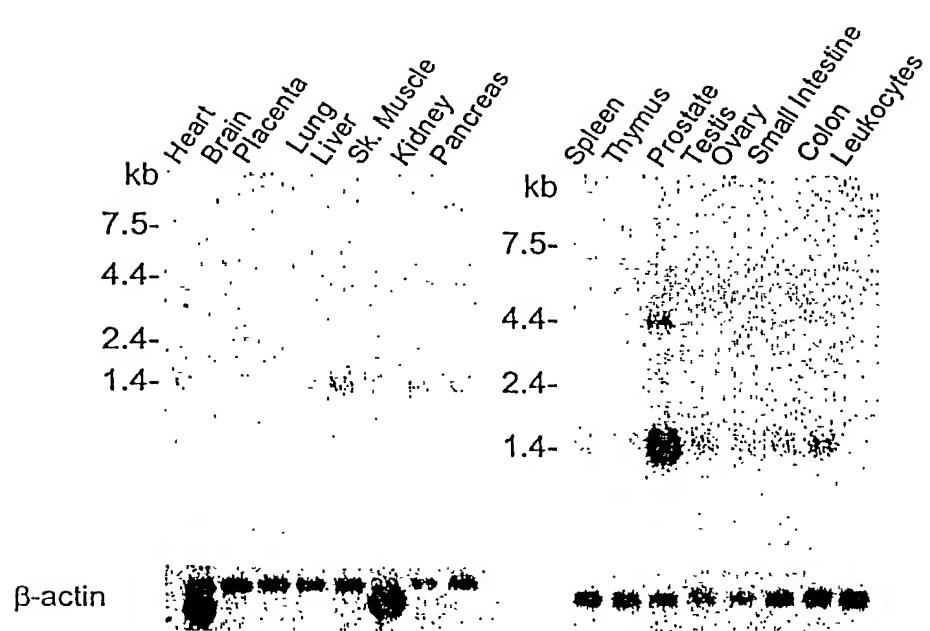
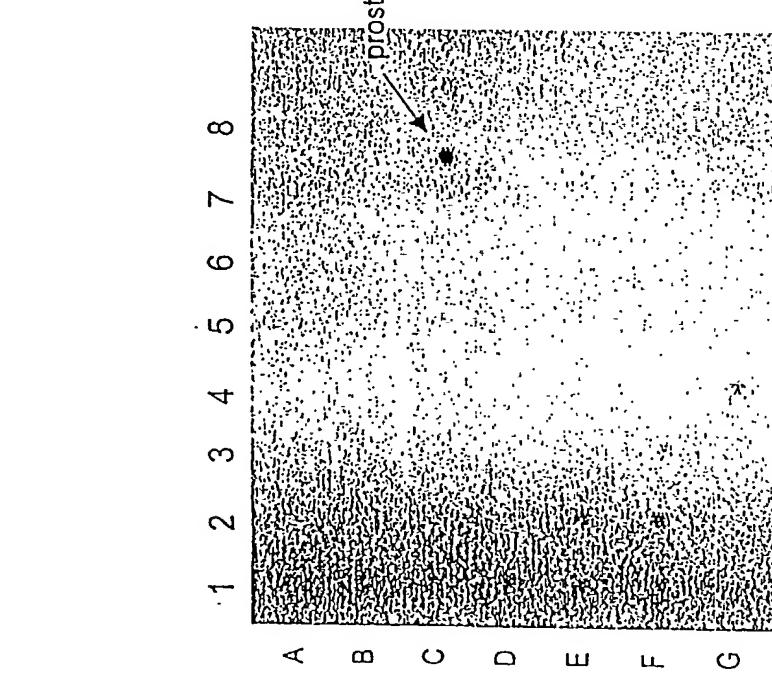


FIG. 3B



A1 brain  
A2 amygdala  
A3 caudate nucleus  
A4 cerebellum  
A5 cerebral cortex  
A6 frontal lobe  
A7 hippocampus  
A8 medulla oblongata

B1 occipital lobe  
B2 putamen  
B3 substantia nigra  
B4 temporal lobe  
B5 thalamus  
B6 sub-thalamic nucleus  
B7 spinal cord

C1 heart  
C2 aorta  
C3 skeletal muscle  
C4 colon  
C5 bladder  
C6 uterus  
C7 prostate  
C8 stomach

D1 testis  
D2 ovary  
D3 pancreas  
D4 pituitary gland  
D5 adrenal gland  
D6 thyroid gland  
D7 salivary gland  
D8 mammary gland

E1 kidney  
E2 liver  
E3 small intestine  
E4 spleen  
E5 thymus  
E6 peripheral leukocytes  
E7 lymph node  
E8 bone marrow

F1 appendix  
F2 lung  
F3 trachea  
F4 placenta

G1 fetal brain  
G2 fetal heart  
G3 fetal kidney  
G4 fetal liver  
G5 fetal spleen  
G6 fetal thymus  
G7 fetal lung

FIG. 4-1

GGGGCCCCCACCTCTGGGCAGCAGCGGAGCCGAGACTCACGGTCAAGCTAAGGCAGAGAGTGGTGGCTGAAGCC  
ATACTATTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACCTTGAAAATGAAGCCTAGG  
AGAAATTAGAAGAACGATTATTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAGACCTGTGCTTTGC  
ATTGCACCAAACAGCCCAGCTGATGAATTGACTGCCCTCAGAACCTCAGCACACACAGGAACCTTTCCACA  
GTGGCACTGCCAATTAAAATAGCTGCTATTATAGCATCTGACTTTCTTACACTCTCTGAGGGAAAGTAATT  
CACCCCTAGCAACTCCCCTCAACAATATTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTGCCAATGG  
TTTCCATCACTCTTGGCATTGGTTACCTGCCAGGTGTGATAGCAGCAATTGTCACACTTCATAATGGAACCAA  
GTATAAGAAGTTCCACATTGGTGGATAAGGGATGTTAACAGAAAGCAGTTGGCTTCAGTTCTTCTTCTTCTT  
GCTGTACTGCATGCAATTATAGCTGTCTTACCAATGAGGCATCCTACAGATAACAAGTTGCTAAACTGGGCAT  
ATCAACAGGTCCAACAAAATAAGAAGATGCCCTGGATTGAGCATGATGTTGGAGAATGGAGATTATGTGTCT  
GGGAATTGTGGATTGGCAATACTGGCTCTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTGACATGG  
AGAGAATTTCACTATATTCAGGTAATAATATAAAAATAACCTAACAGGTAATCTCTTTGTGTTATGAT  
ATAGAATATGTTGACTTACCCATAAAAATAACAAATGTTTCAACAGCAAAGATCTTACACTTGTCCAATT  
AATAATGTGCTCTCCTGTTGTTCCCTATTGCTTAATTAGGACAAGTGTTCCTAGACATAAAATAAAAGGCAT  
AAAAATATTCTTGTTTTTTTTTGTTGTTGTTGTTGTTGTTGTTGTTGAGATGAAGTCTCG  
CTCTGTTGCCATGCTGGAGTACAGTGGCACGATCTGGCTCACTGCAACCTGCCCTGGTCAAGGCATT  
TCTTGCTCAGCCTCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCAGCTAATTGTTGTTAGTA  
GAGACAGGGTTTCCCATGTTGGCCAGGCTGGCTCGATCTCCTGACCTCAAATGATCCGCCACCTGGCCTCCC  
AAAGTGCTGGATGACAGTTGTGAGCCACCAACTCAGCCTGCTTTCTAATATTGAAACTTGTAGACAATT  
GCTACCCATCTAATGTGATATTAGGAATCCAATATGCACTGGTTATTATTCTTAAAAAAATATTCTTAC  
TGTACCTGAATTAGTAATGCCCTTATGTTACACAACCTAGCACTTCCAGAAACAAAAACTCTCCTTGAAA  
TAATAGAGTTTATCTACCAAGATATGCTAGTGTCATTCAAAGGCTGCTTTCCAGCTACATTAT  
ACTTACTCACTGAAGTTCTAAATATTCTGTAATTAAAACATCTCAGATTACTGAGGTTATCTCTGGT  
GGTAGATTATCCATAAGAAGAGTGTGCCAGAATCACTCTGGATCCTGTCAGACAAGATTCAAAGGACTAAA

FIG. 4-2

TTTAAATTCAAGTCATGAAACACTGCCAATTACCGTTATGGGTAGACATCTTGGAAATTCCACAAGGTAGACATT  
CGCAACTATCCCTTACATGTCCACACGTATACTCCAACACTTATTAGGCATCTGATTAGTTGGAAAGTATGC  
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTCTAATTTCCTAATTGTAGGTTAG  
CCTGATAACCACGGAGTTCTTGGTCTCATTAAATAGCTTCTCACACATTGCTCTGCCTGTTACACATATGA  
TGAACACTGCTTTAGACTTCACTAGGAATTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA  
ATACCTAGCCCATAATAGGTATAACATACACATTGGTAAAACTAATTTCACCAATGACATGTATTTCACACT  
AGTAACCTAGAAATGTTCACTAAAATCTGAGAACTGGTTACACTACAAAGTTACCTGGAGATTCAATATGAAA  
ACGCAAACCTAGCTATTGATTGATTCACTGGACTTAAGAATGCCCTGAATAATTGTGAGTCGATTGTTCT  
GGCAGGCTAATGACCATTCCAGTAAAGTGAATAGAGGTCAAGTCGTTACACTACAAAGGGTTGTCAGAACACCGT  
TGAGATTACATAGGTGAACAACTATTTAAGCAACTTTATTGTGAGTCAGACATTGAAAAAATTGTTCAATTATTCATGTTATC  
AGAATATTGATTTTAAACATAGGCCAGTTCAACTGATAAGATCACTGAAGTCAAATTGATTTGCTATAATCTCAATCTACCTATAT  
CATTAGTCGCCCTCACAACTGATAAGATCACTGAAGTCAAATTGATTTGCTATAATCTCAATCTACCTATAT  
TTAATTGAGAATCTAAATGTACAAATCATTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGCCCT  
GATTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGGACAAAAAAATAATCATAAG  
GGGATGAACAAATGGTGGAGAAAGAGTAGACAAAGTTGATCACCTGCCCTCAAGAAAGGCTGTGAATTTC  
TTCACCTAGACAGCTGGAGACAAGAAATTACCCAAAGTAAGGTGAGGAGGATAGGCAAAAGAGCAGAAAGATG  
TGAATGGACATTGTTGAGAAATGTGATAGGAAACAATCATAGATAAAGGATTCCAAGCAACAGAGCATATCCAG  
ATGAGGTTAGGATGGGATAAAACTCTTATTGAACCAATCTCACCAATTGTTCTTGCAGAGCAAGCTAGGA  
ATTGTTCCCTTACTGGCACAATACACGATTGATTTGCCCTGAATAAGTGGATAGATATAAAACAATTG  
TATGGTATACACCTCAACTTTATGATAGCTGTTCCCTGAATTGTTGCTGATATTAAAGCATACTATT  
CCTGCCATGCTTGAGGAAGAAGACTGAAGATTAGACATGGTGGAAAGACGTACCAAAATTAAACAAACTGAG  
ATATGTTCCAGTTGAGAATTACTGTTACACACATTGTTCAATATTGATATATTGATCACCAACATTCA  
AGTTGTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAA (SEQ ID NO:6)

# FIG. 5

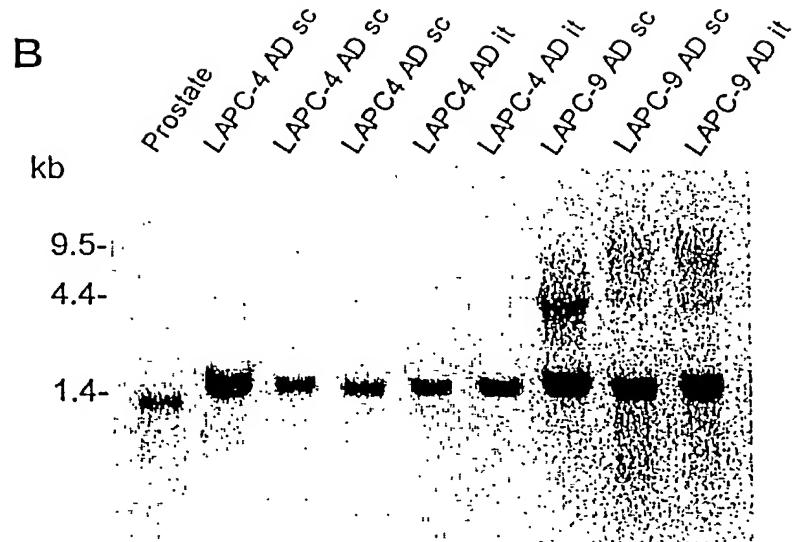
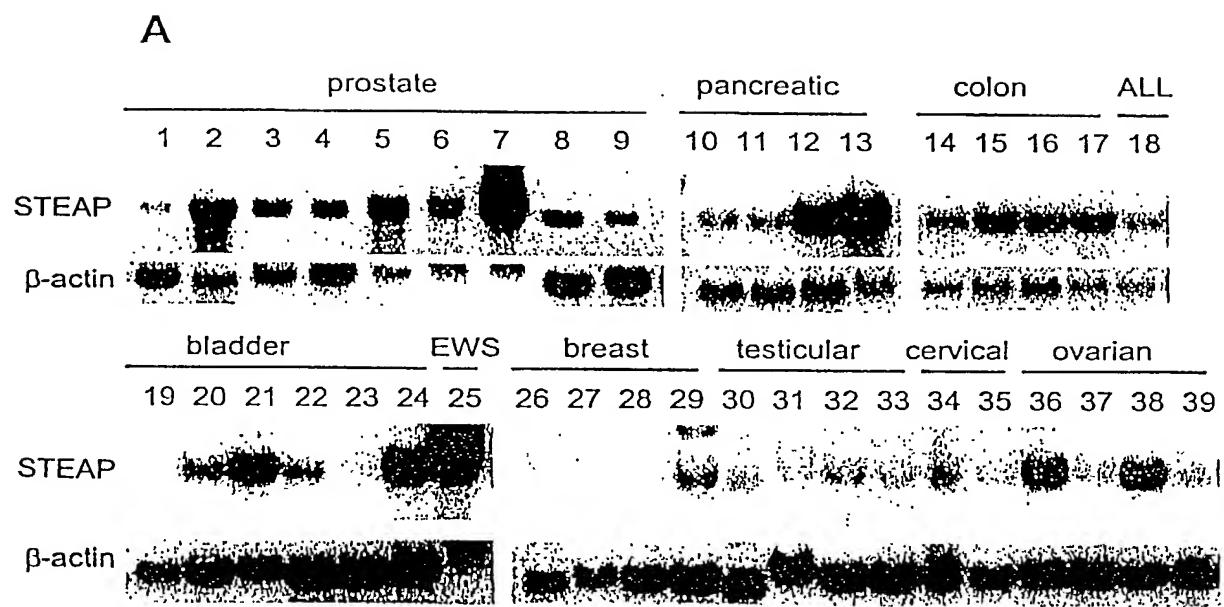
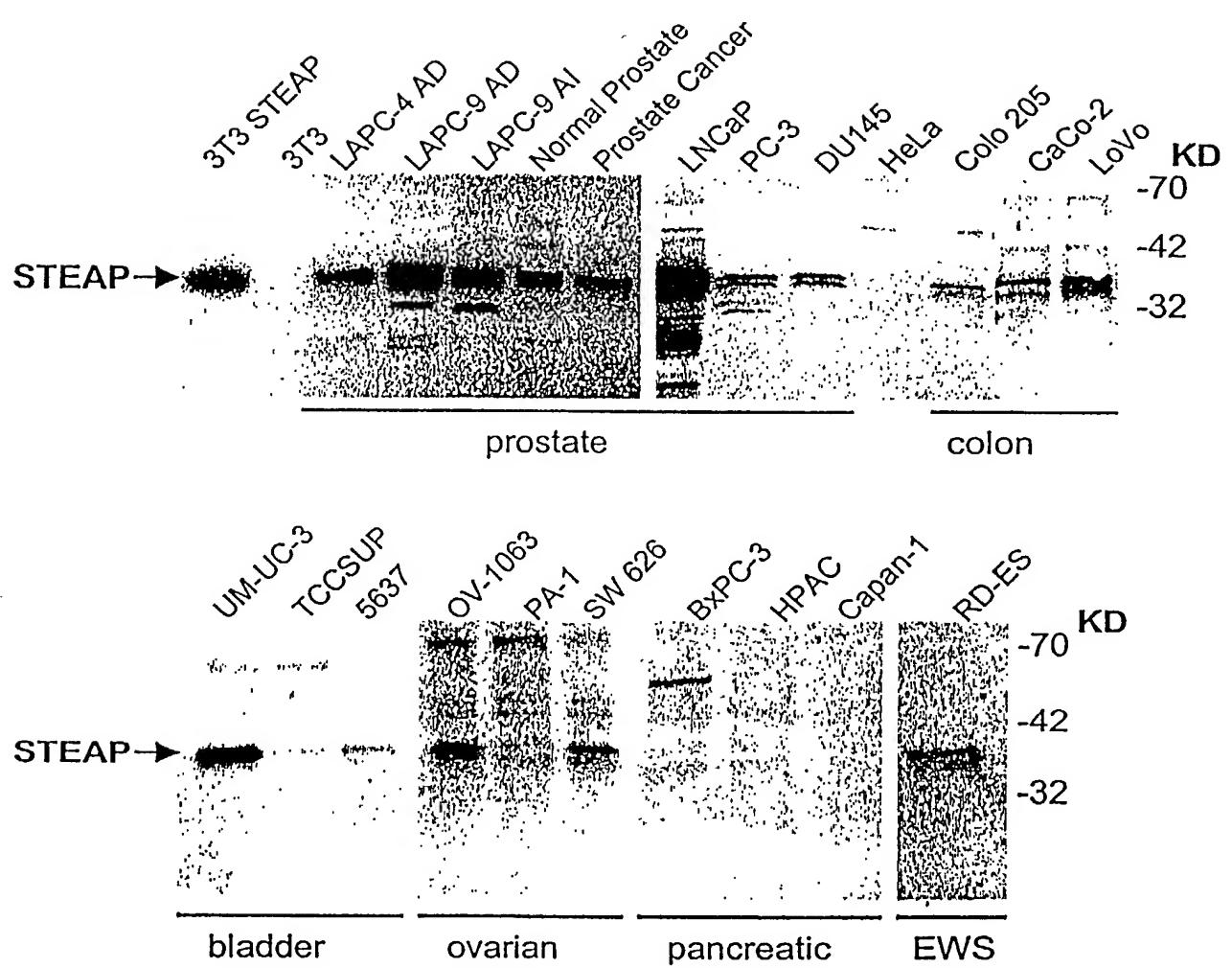
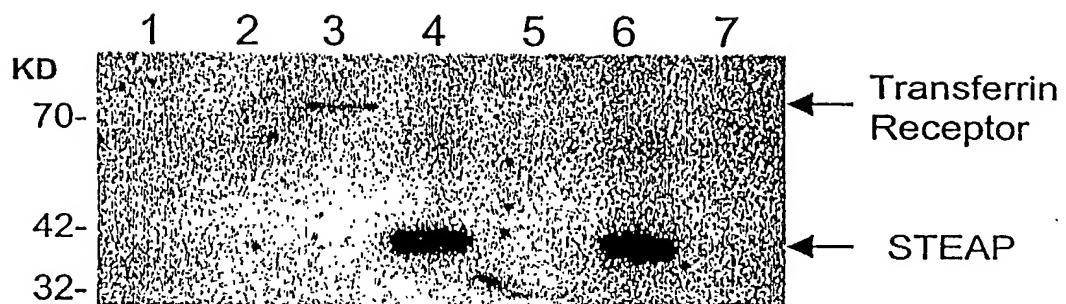


FIG. 6



**FIG. 7**

**A**



**B**

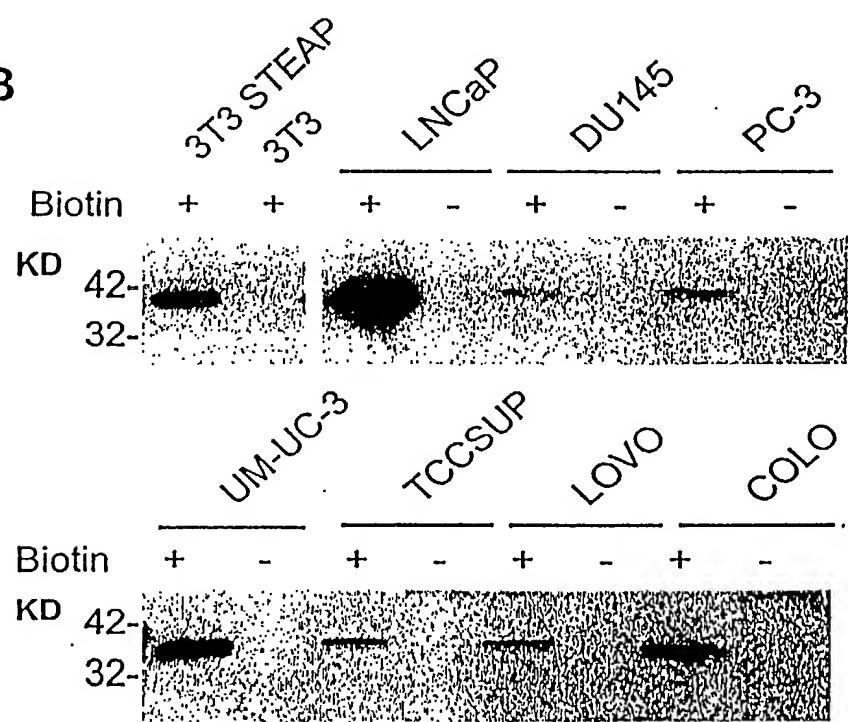


FIG. 9

	10	19	28	37	46	55												
5'	GAC	TTT	TAC	AAA	ATT	CCT	ATA	GAG	ATT	GTG	AAT	AAA	ACC	TTA	CCT	ATA	GTT	GCC
	Asp	Phe	Tyr	Lys	Ile	Pro	Ile	Glu	Ile	Val	Asn	Lys	Thr	Leu	Pro	Ile	Val	Ala
	64								82			91			100			109
	ATT	ACT	TTG	CTC	TCC	CTA	GTA	TAC	CTC	GCA	GGT	CTT	CTG	GCA	GCT	GCT	TAT	CAA
	Ile	Thr	Leu	Leu	Ser	Leu	Val	Tyr	Leu	Ala	Gly	Leu	Leu	Ala	Ala	Ala	Tyr	Gln
	118								136			145			154			163
	CTT	TAT	TAC	GGC	ACC	AAG	TAT	AGG	AGA	TTT	CCA	CCT	TGG	TTG	GAA	ACC	TGG	TTA
	Leu	Tyr	Tyr	Gly	Thr	Lys	Tyr	Arg	Arg	Phe	Pro	Pro	Trp	Leu	Glu	Thr	Trp	Leu
	172								190			199			208			217
	CAG	TGT	AGA	AAA	CAG	CTT	GGA	TTA	CTA	AGT	TTT	TTC	TTC	GCT	ATG	GTC	CAT	GTT
	Gln	Cys	Arg	Lys	Gln	Leu	Gly	Leu	Leu	Ser	Phe	Phe	Ala	Met	Val	His	Val	
	226				235				244			253			262			271
	GCC	TAC	AGC	CTC	TGC	TTA	CCG	ATG	AGA	AGG	TCA	GAG	AGA	TAT	TTG	TTT	CTC	AAC
	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	Glu	Arg	Tyr	Leu	Phe	Leu	Asn
	280				289				298			307			316			325
	ATG	GCT	TAT	CAG	CAG	GTT	CAT	GCA	AAT	ATT	GAA	AAC	TCT	TGG	AAT	GAG	GAA	GAA
	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu
	334				343				352			361			370			379
	GTT	TGG	AGA	ATT	GAA	ATG	TAT	ATC	TCC	TTT	GGC	ATA	ATG	AGC	CTT	GGC	TTA	CTT
	Val	Trp	Arg	Ile	Glu	Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu
	388				397				406			415			424			433
	TCC	CTC	CTG	GCA	GTC	ACT	TCT	ATC	CCT	TCA	GTG	AGC	AAT	GCT	TTA	AAC	TGG	AGA
	Ser	Leu	Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	Arg
	442				451				460			469			478			487
	GAA	TTC	AGT	TTT	ATT	CAG	TCT	ACA	CTT	GGA	TAT	GTC	GCT	CTG	CTC	ATA	AGT	ACT
	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	Leu	Ile	Ser	Thr
	496				505				514									
	TTC	CAT	GTT	TTA	ATT	TAT	GGA	TGG	AAA	CGA	GCT	3'	(SEQ ID NO:7)					
	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	(SEQ ID NO:8)						

## FIG. 10

STEAP-2, AA508880 (NCI\_CGAP Pr6)

ggtcgactttcccttattcccttgcagagatctgattcatccatatgctagaaaccaacagagtgactttaca  
aaattctatagagattgtgataaaaacccctacctatagttgcattactttgtctccctagtataaccttgagg  
tcttcggcagctgtttatcaactttacccggcaccaggataggagattttcaccccttgcgttggaaacctggta  
cagttagaaaaacagctggattactaaggttgttctcgatggccatgttgcctacaggctctgcttaccga  
tgagaaggcagagat (SEQ ID NO:9)

STEAP-2, 98P4B6 SSH fragment

TTTGCAGCTTCAGATAACCCAGACTGAGCTGGAACCTGGAAATTGTCTTCCTATTGACTCTACTTCTTAAAGCG  
GCTGCCATTACATTCTCAGCTGTCCTTGCAGTTACGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC  
TCCTCAAAGGAAGGCAGCATGTGTCCTTTT (SEQ ID NO:10)

AI139607 (testis EST)

aagaaggagaatccatattagcacccctcagccgtcagtgattcatatgtggctttggaaatactgggtttt  
ttctgttttactttggaaatcacttcttgcattgttagcaatgcagtcactggagagatccgattttgt  
ccagtcacaaactgggttatttgcacccgtatcttgtacagccacacccctgggtacggggaaagagattcctc  
agcccttcaatctcagatggatcttcctgcagcctacgtgttagggcttatcatccctgcactgtgtggta  
tcaagttgtcataatcatgcattgttagacaacacccctacaaggatccggcagggtggggaaaggaactcaaa  
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagtcaatttagctggaaaaaaaaa (SEQ ID NO:11)

R80991 (placental EST)

ggccgcggcancgcctacgacccgttgcacccctggcagtcacgggtttggccanacaagagccacccctgggtg  
aaggaggaggctggcgatggagatctacccctccctggagtgctggccctggcaccgttgcctctgtggcc  
tgacccactggccattgcaactcgctcaactggagggagttcagcttcgttgcgttgcactggcttgc  
ggccntcgtgctgagcacactncacacgctcacctacggctggaccggcgcctcggaggagagccgtacaagttc  
tacccntccctccacccctcacgntcacgtgtggccctgcgttgcattcctggccaaagccctgtttntac  
tgccttgcattcagccgnaga (SEQ ID NO:12)

## FIG. 11A

STEAP-1	106	FYKIPILVINKVLPMVSITLLALVYLPGVIAAIQLHNGTKYKKFPHWLDKWMLTRKQFG
STEAP-2	2	FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG
	*****	*****
STEAP-1	166	LLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIV
STEAP-2	62	LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEVWRRIEMYISFGIM
	*****	*****
STEAP-1	226	GLAILALLAVTSIPSVDSDLTWREFHYIQSKLGIVSLLGTIHALIFAWNK
STEAP-2	122	SLGLLSLLAVTSIPSVDSDLTWREFHYIQSTLGYVALLISTFHVLIVGWKR
	*****	*****

(Portion of SEQ ID NO:2)

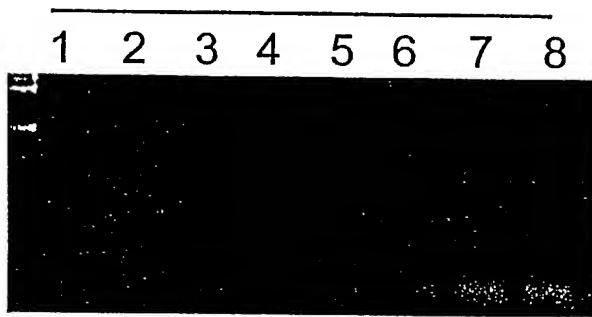
(Portion of SEQ ID NO:8)

FIG. 11B

1	15 16	30 31	45 46	60 61	75 76	90
STEAP-1	MESRDIDTINQEENK	MDPRMFLFEDDYLK	DGETSMKRPVLLH	LQTHAHADEFDCPSE	LQTHQELFQWHLPI	KIAIASLTFITL
STEAP-2	-----	-----	-----	-----	-----	90
STEAP-3	-----	-----	-----	-----	-----	0
STEAP-4	-----	-----	-----	-----	-----	0
91	105 106	120 121	135 136	150 151	165 166	180
STEAP-1	LPEVTHPLATSEQQY	FYKQPTI	YVTKYLPY	EYHLDKAMLTTRKQG	EISFFPAVLAHATKSL	-----
STEAP-2	-----D	-----D	-----D	-----D	-----D	76
STEAP-3	-----	-----	-----	-----	-----	0
STEAP-4	-----	-----	-----	-----	-----	0
181	195 196	210 211	225 226	240 241	255 256	270
STEAP-1	SPPRSRSPYFCEAM	AYQQVQONKEDAWIE	ADYVREMEIYTSGLY	GIAILIAVATSIQS	VPSDLIWFREFIQSQ	KLGTVLISLTLTIAH
STEAP-2	CLPPRSRSPYFCEAM	AYQQVQANIEINSWNE	EYVWRIEATISFGIM	SIGLISLAVATSIQS	VSNALANWREFSEFIQS	TUGYVAMLISLTHVTL
STEAP-3	-----	-----TKKENPST	SSAWLSDSYVALGIL	GPFKFLIGITSLPS	VSNAVNWFREFEVQSQ	KLGTVLILQIQTHTL
STEAP-4	-----ATTKSTW	QSSRSWPXKSHLMYK	EYVFRMEIYLSLGT	ALGTLISLAVATSIQS	IANSIATWREFSEFIQS	SIGLTVLXPLSTLTHI
271	285 286	300 301	315 316	330 331	345 346	360
STEAP-1	IPAWKWDIDIKQFWW	YI <del>PPPT</del> IAVLPYV	YI <del>PPPT</del> ISLILPCK	KIKIKIRH <del>G</del> PDVTKI	NTEICSQL	339 (SEQ ID NO:2)
STEAP-2	-----	-----	-----	-----	-----	173 (SEQ ID NO:8)
STEAP-3	VYGGKRFPLSPSLRW	YLPAAVVLGLIIPCT	YI <del>PPPT</del> APCVDN	TLTRI <del>Q</del> GRFERNSKH	-----	128 (Portion of SEQ ID NO:2)
STEAP-4	TYGWTRAFFEEESRYKF	YI <del>PPPT</del> ITXLLVPCV	YI <del>PPPT</del> ALFXLPCIQ	P-----	-----	128 (Portion of SEQ ID NO:8)

FIG. 14A

26x



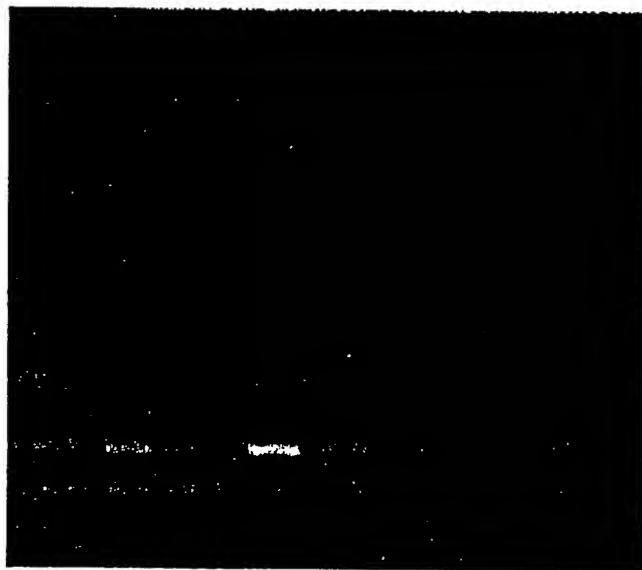
- 1. Brain
- 2. Prostate
- 3. LAPC-4 AD
- 4. LAPC-4 AI
- 5. LAPC-9 AD
- 6. HeLa
- 7. Murine cDNA
- 8. Neg control

FIG. 14B

1 2 3 4 5 6 7 8

25x

30x



- 1. Colon
- 2. Ovary
- 3. Leukocytes
- 4. Prostate
- 5. Small Intestine
- 6. Spleen
- 7. Testis
- 8. Thymus

FIG. 15A

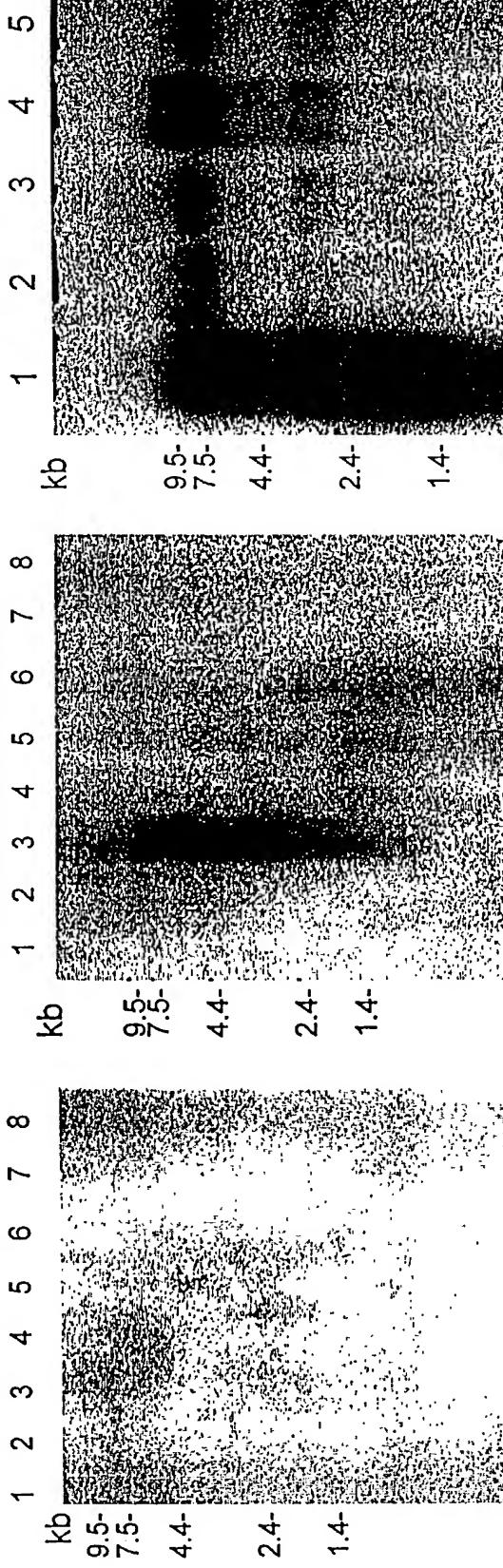


FIG. 15B

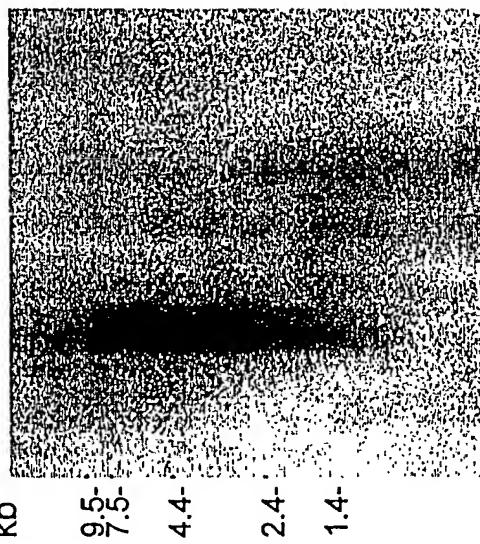
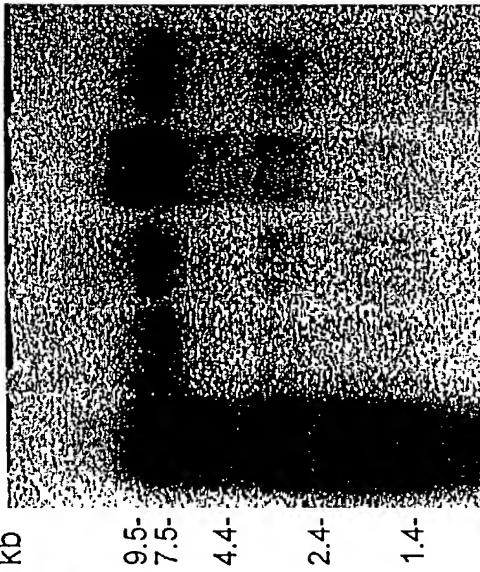


FIG. 15C



- 1. Heart
- 2. Brain
- 3. Placenta
- 4. Lung
- 5. Liver
- 6. Skeletal Muscle
- 7. Kidney
- 8. Pancreas

- 1. Spleen
- 2. Thymus
- 3. Prostate
- 4. Testis
- 5. Ovary
- 6. Small Intestine
- 7. Colon
- 8. Leukocytes

- 1. Prostate
- 2. LAPC-4 AD
- 3. LAPC-4 AI
- 4. LAPC-9 AD
- 5. LAPC-9 AI

FIG. 16

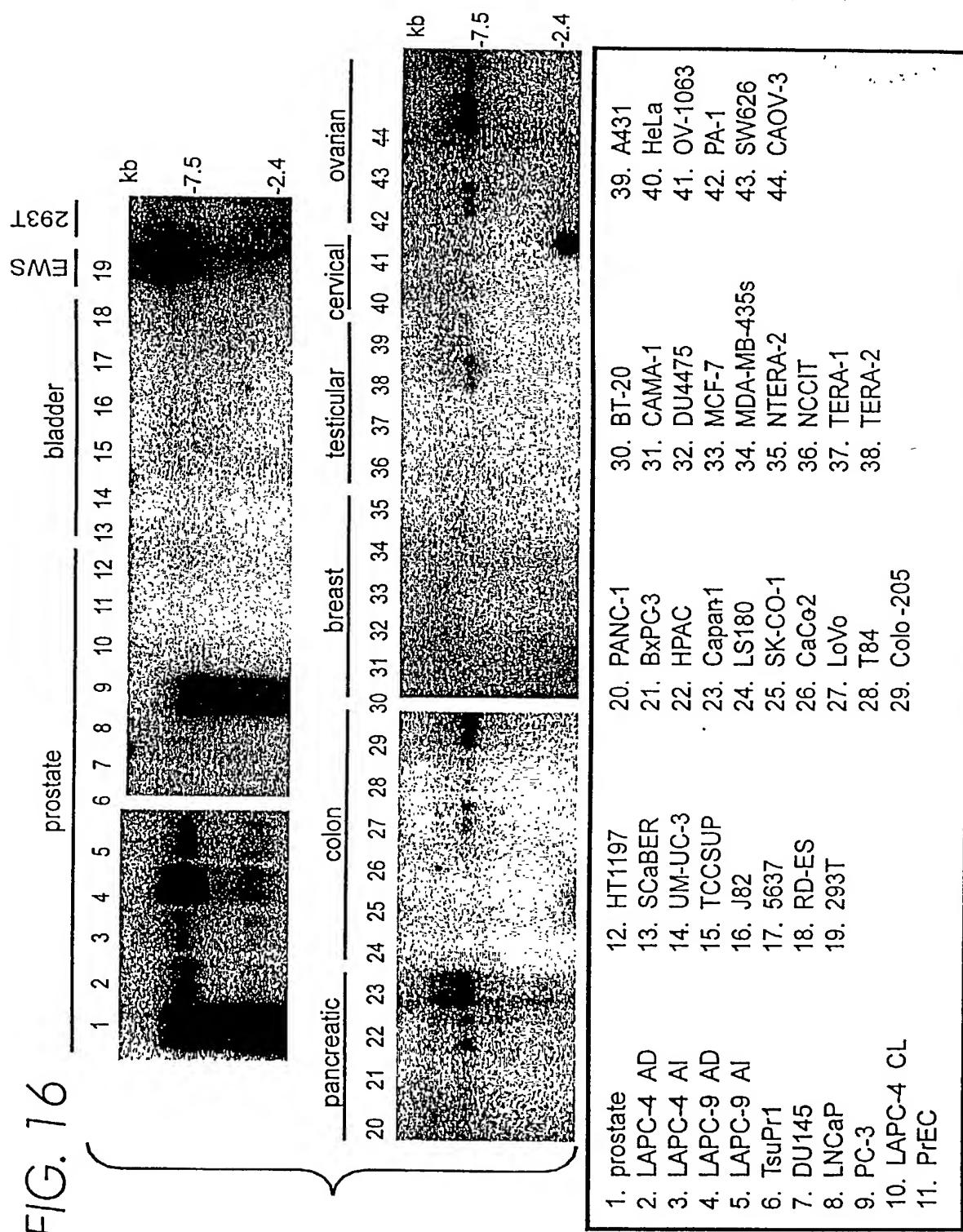


FIG. 17

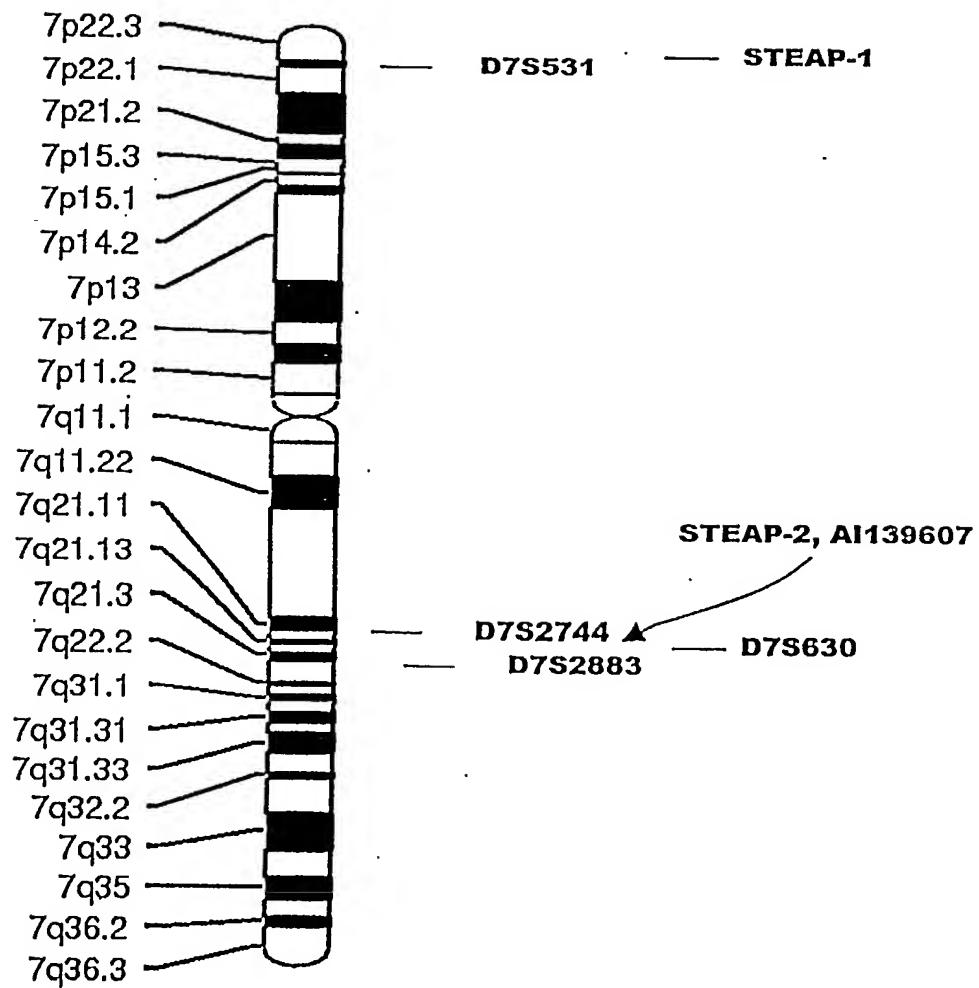
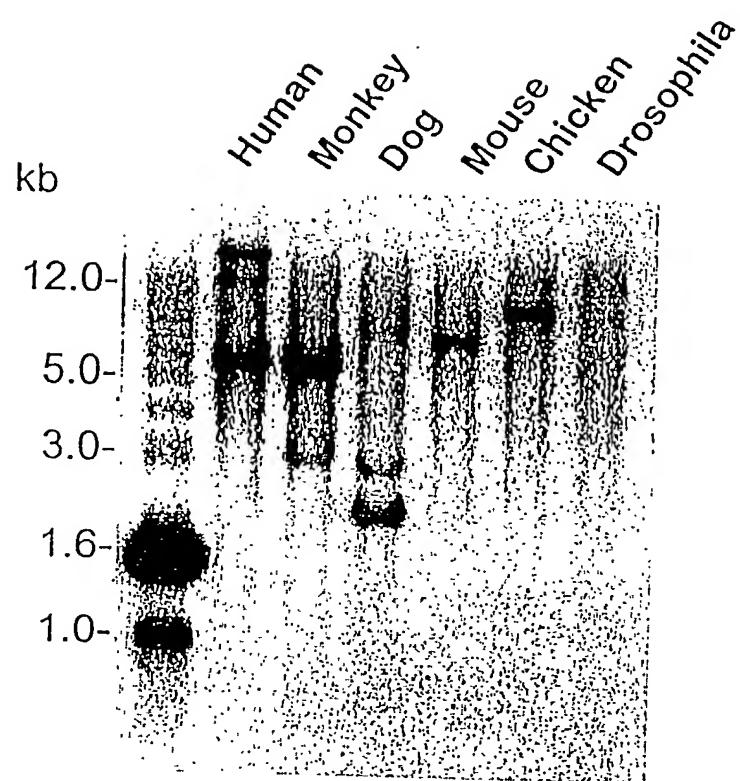
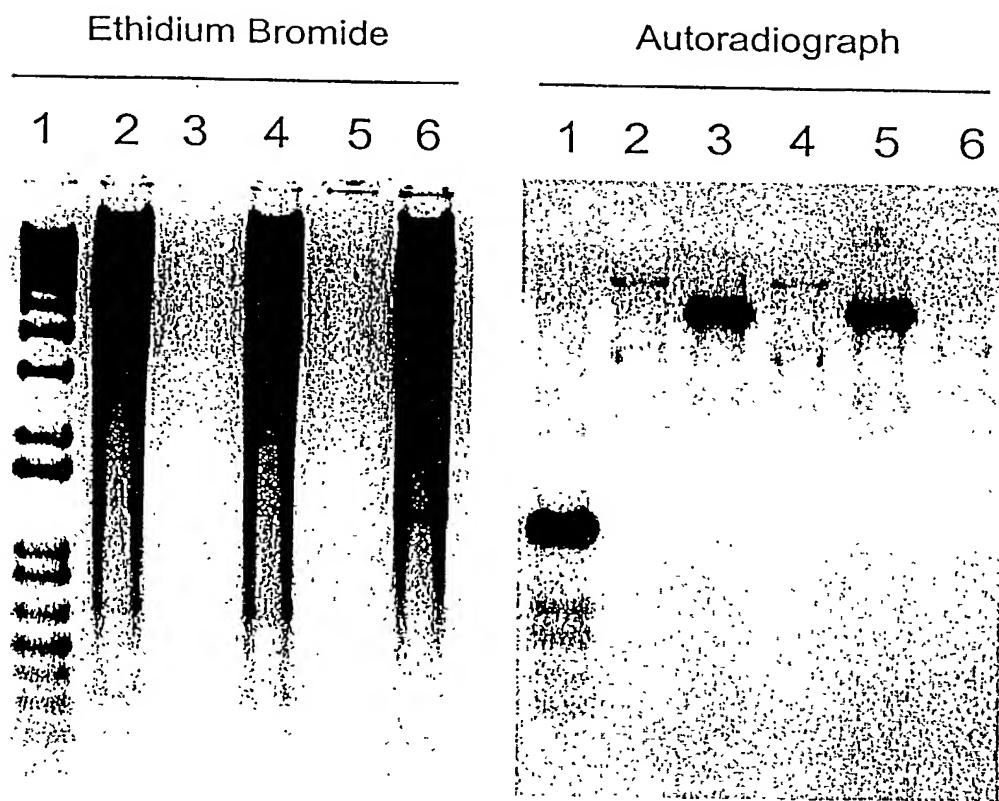


FIG. 19



**FIG. 20**



**Lanes**

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3